

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

1-22. (cancelled)

23. (currently amended) A purified HIV-1 variant virus,

wherein said HIV-1 variant virus differs at the amino acid sequence level from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in the entire Pol protein, and 13.0% in the entire Env protein,

wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said HIV-1 variant virus,

wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641,

wherein the genetic structure of said HIV-1 variant is 5'-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3', and

wherein the nucleic acid of said HIV-1 variant virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe comprising the genomic cDNA of HIV-1_{MAL}.

24. (cancelled)

25. (previously presented) The HIV-1 variant virus of claim 23, wherein the nucleic acid of said HIV-1 variant virus can be detected by hybridization with a DNA probe comprising a restriction enzyme fragment of the cDNA of HIV-1_{MAL}, and wherein the restriction enzyme is selected from the group consisting of *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HincII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*.

26. (withdrawn) A purified HIV-1 variant virus,
wherein said HIV-1 variant virus differs genetically from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4 % in Gag, 3.1% in Pol, and 13.0% in Env, and from HIV-1_{BRU} by at least 20.7% in Env,
wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said HIV-1 variant virus, and
wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641.

27. (withdrawn) A purified HIV-1 variant virus,
wherein said HIV-1 variant virus differs genetically from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4 % in Gag, 3.1% in Pol, and 13.0% in Env, and from HIV-1_{BRU} by at least 9.8 % in Gag,

wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said HIV-1 variant virus, and

wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641.

28. (withdrawn) A purified HIV-1 variant virus,

wherein said HIV-1 variant virus differs genetically from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4 % in Gag, 3.1% in Pol, and 13.0% in Env, and from HIV-1_{BRU} by at least 5.5% in Pol,

wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said HIV-1 variant virus, and

wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641.

29. (withdrawn) A purified HIV-1 variant virus,

wherein said HIV-1 variant virus differs genetically from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4 % in Gag, 3.1% in Pol, and 13.0% in Env, and from HIV-1_{BRU} by at least 9.8 % in Gag, 5.5% in Pol, and 20.7% in Env,

wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said HIV-1 variant virus, and

wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641.

30. (withdrawn) The HIV-1 variant virus of claim 29, wherein said HIV-1 variant virus differs genetically from HIV-1_{MAL} by 0-10.8% in Gag, 0%-8.4% in Pol, and 0%-19.8% in Env.

31. (withdrawn) The HIV-1 variant virus of claim 30, wherein said virus is HIV-1_{MAL}.

32. (withdrawn) The HIV-1 variant virus of claim 30, wherein said virus is HIV-1_{ELI}.

33. (withdrawn) The HIV-1 variant virus of any one of claims 26-30, wherein the nucleic acid of said HIV-1 variant virus can be detected by hybridization with a DNA probe selected from the group of nucleic acids consisting of the genomic cDNA of HIV-1_{MAL} and restriction enzyme fragments of the cDNA of HIV-1_{MAL}, and wherein the restriction enzyme is selected from the group consisting of *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HincII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*.

34. (withdrawn) A purified HIV-1 variant virus,
wherein said HIV-1 variant virus differs genetically from HIV-1_{BRU} by at least
21.7% in Env,
wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of
said HIV-1 variant virus, and
wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus
designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE
MICRO-ORGANISMES (CNCM) under No. I-641.

35. (withdrawn) A purified HIV-1 variant virus,
wherein said HIV-1 variant virus differs genetically from the group of viruses
consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4 % in Gag, 3.1% in Pol,
and 13.0% in Env, and from HIV-1_{BRU} by at least 12.0 % in Gag,
wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of
said HIV-1 variant virus, and
wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus
designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE
MICRO-ORGANISMES (CNCM) under No. I-641.

36. (withdrawn) A purified HIV-1 variant virus,

wherein said HIV-1 variant virus differs genetically from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4 % in Gag, 3.1% in Pol, and 13.0% in Env, and from HIV-1_{BRU} by at least 7.7% in Pol,

wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said HIV-1 variant virus, and

wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641.

37. (withdrawn) A purified HIV-1 variant virus,

wherein said HIV-1 variant virus differs genetically from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4 % in Gag, 3.1% in Pol, and 13.0% in Env, and from HIV-1_{BRU} by at least 9.8 % in Gag, 5.5% in Pol and 20.7% in Env,

wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said HIV-1 variant virus, and

wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus designated HIV-1_{MAL} deposited at a the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641.

38. (withdrawn) The HIV-1 variant virus of any one of claims 34-37, wherein the nucleic acid of said HIV-1 variant virus can be detected by hybridization with a DNA

probe selected from the group of nucleic acids consisting of the genomic cDNA of HIV-1_{MAL} and restriction enzyme fragments of the cDNA of HIV-1_{MAL}, and wherein the restriction enzyme is selected from the group consisting of *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HincII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*.

39. (withdrawn) A purified HIV-1 variant virus of claim 23,
wherein said HIV-1 variant virus differs at the amino acid sequence level from the group of viruses consisting of HIV-1_{IIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} at least 9.8% in the entire Gag protein, 5.5% in the entire Pol protein, and 20.7% in the entire Env protein,
wherein antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said HIV-1 variant virus,
wherein said antibodies bind to Gag, Pol, or Env polypeptides of the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641, and
wherein the genetic structure of said HIV-1 variant is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3'.

40. (withdrawn) The HIV-1 variant virus of claim 39, wherein the nucleic acid of said HIV-1 variant virus can be detected by hybridization with a DNA probe comprising the genomic cDNA of HIV-1_{MAL}.

41. (withdrawn) The HIV-1 variant virus of claim 39, wherein the nucleic acid of said HIV-1 variant virus can be detected by hybridization with a DNA probe comprising a restriction enzyme fragment of the cDNA of HIV-1_{MAL}, and wherein the restriction enzyme is selected from the group consisting of *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HincII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*.

42. (cancelled)

43. (previously presented) The HIV-1 variant virus of claim 23, wherein said HIV-1 variant virus differs genetically from HIV-1_{MAL} by 0-10.8% in Gag, 0%-8.4% in Pol, and 0%-19.8% in Env.

44. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Env sequence of HIV-1_{MAL} as shown in Figure 3.

45. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Gag sequence of HIV-1_{MAL} as shown in Figure 3.

46. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Pol sequence of HIV-1_{MAL} as shown in Figure 3.

47. (withdrawn) A purified HIV-1 variant virus,

wherein the nucleic acid of said HIV-1 variant virus said HIV-1 variant virus is complementary to the nucleic acid of HIV-1_{MAL} deposited with the CNCM as deposit number I-641, and wherein the nucleic acid of the HIV-1 variant virus hybridizes to the HIV-1_{MAL} nucleic acid under stringent conditions (50% formamide, 5X SSC, at 42°C, for 12-16 hours).

48. (new) A purified human immunodeficiency virus designated LAV_{MAL}, wherein said LAV_{MAL} virus differs at the amino acid sequence level from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in the entire Pol protein, and 13.0% in the entire Env protein;

antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said LAV_{MAL} virus;

said antibodies bind to Gag, Pol, or Env polypeptides of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5'-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe comprising the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641; and

the genome of said LAV_{MAL} virus comprises at least one restriction site of the restriction map shown in Fig. 1.

49. (new) The purified human immunodeficiency virus designated LAV_{MAL} of claim 48, wherein the genome of LAV_{MAL} has the restriction map shown in Fig. 1.

50. (new) A purified human immunodeficiency virus designated LAV_{MAL}, wherein said LAV_{MAL} virus differs at the amino acid sequence level from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in the entire Pol protein, and 13.0% in the entire Env protein;

antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said LAV_{MAL} virus;

said antibodies bind to Gag, Pol, or Env polypeptides of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe comprising the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641; and

said LAV_{MAL} virus comprises a protein or glycoprotein encoded by at least one of the following LAV_{MAL} cDNA sequences of Fig 3E: 1 to 530; 34-530; and 531-877.

51. (new) A purified human immunodeficiency virus designated LAV_{MAL}, wherein said LAV_{MAL} virus differs at the amino acid sequence level from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in the entire Pol protein, and 13.0% in the entire Env protein;

antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said LAV_{MAL} virus;

said antibodies bind to Gag, Pol, or Env polypeptides of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe comprising the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641; and

said LAV_{MAL} virus comprises a protein or glycoprotein encoded by at least one of the following LAV_{MAL} cDNA sequences of Fig 3E: 37-130, 211-289, 488-530, 490-620, and 680-700.

52. (new) A purified human immunodeficiency virus designated LAV_{MAL}, wherein said LAV_{MAL} virus differs at the amino acid sequence level from the group of viruses consisting of HIV-1_{IIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in the entire Pol protein, and 13.0% in the entire Env protein; antibodies in AIDS patient sera bind to Gag, Pol, or Env polypeptides of said LAV_{MAL} virus;

said antibodies bind to Gag, Pol, or Env polypeptides of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe comprising the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641, or a restriction enzyme fragment thereof, wherein the restriction enzyme is selected from at least one of the group consisting of *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HincII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*; and

the genome of said LAV_{MAL} virus comprises at least one restriction site of the restriction map shown in Fig. 1.